OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/975,123

DATE: 11/01/2001
TIME: 08 41:48

Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\11012001\I975123.raw**

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  3  <110> APPLICANT: Susan M. Freier
  6  <120> TITLE OF INVENTION: ANTISENSE MODULATION OF INSULIN-LIKE GROWTH FACTOR BINDING
PROTEIN 5
  7         EXPRESSION
  9  <130> FILE REFERENCE: RTS-0253
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/975,123
C--> 11 <141> CURRENT FILING DATE: 2001-10-09
 11  <160> NUMBER OF SEQ ID NOS: 43
 14  <210> SEQ ID NO: 1
 15  <211> LENGTH: 20
 16  <212> TYPE: DNA
 17  <213> ORGANISM: Artificial Sequence
 19  <220> FEATURE:
 21  <223> OTHER INFORMATION: Antisense Oligonucleotide
 23  <400> SEQUENCE: 1
 24  tccgtcatcg ctcctcaggg                                              20
 27  <210> SEQ ID NO: 2
 28  <211> LENGTH: 20
 29  <212> TYPE: DNA
 30  <213> ORGANISM: Artificial Sequence
 32  <220> FEATURE:
 34  <223> OTHER INFORMATION: Antisense Oligonucleotide
 36  <400> SEQUENCE: 2
 37  atgcattctg ccccaagga                                               20
 40  <210> SEQ ID NO: 3
 41  <211> LENGTH: 1612
 42  <212> TYPE: DNA
 43  <213> ORGANISM: Homo sapiens
 45  <220> FEATURE:
 47  <220> FEATURE:
 48  <221> NAME/KEY: CDS
 49  <222> LOCATION: (44)...(862)
 51  <400> SEQUENCE: 3
 52  ctctcctgcc ccaccccgag gtaaaggggg cgactaagag aag atg gtg ttg ctc      55
 53                                                 Met Val Leu Leu
 54                                                  1
 56  acc gcg gtc ctc ctg ctg ctg gcc gcc tat gcg ggg ccg gcc cag agc     103
 57  Thr Ala Val Leu Leu Leu Leu Ala Ala Tyr Ala Gly Pro Ala Gln Ser
 58   5                   10                  15                  20
 60  ctg ggc tcc ttc gtg cac tgc gag ccc tgc gac gag aaa gcc ctc tcc    151
 61  Leu Gly Ser Phe Val His Cys Glu Pro Cys Asp Glu Lys Ala Leu Ser
 62                   25                  30                  35
 64  atg tgc ccc ccc agc ccc ctg ggc tgc gag ctg gtc aag gag ccg ggc    199
 65  Met Cys Pro Pro Ser Pro Leu Gly Cys Glu Leu Val Lys Glu Pro Gly
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 72 gtc tac acc gag cgc tgc gcc cag ggg ctg cgc tgc ctc ccc cgg cag       295
 73 Val Tyr Thr Glu Arg Cys Ala Gln Gly Leu Arg Cys Leu Pro Arg Gln
 74        70                  75                  80
 76 gac gag gag aag ccg ctg cac gcc ctg ctg cac ggc cgc ggg gtt tgc       343
 77 Asp Glu Glu Lys Pro Leu His Ala Leu Leu His Gly Arg Gly Val Cys
 78 85                  90                  95                 100
 80 ctc aac gaa aag agc tac cgc gag caa gtc aag atc gag aga gac tcc       391
 81 Leu Asn Glu Lys Ser Tyr Arg Glu Gln Val Lys Ile Glu Arg Asp Ser
 82                105                 110                 115
 84 cgt gag cac gag gag ccc acc acc tct gag atg gcc gag gag acc tac       439
 85 Arg Glu His Glu Glu Pro Thr Thr Ser Glu Met Ala Glu Glu Thr Tyr
 86                120                 125                 130
 88 tcc ccc aag atc ttc cgg ccc aaa cac acc cgc atc tcc gag ctg aag       487
 89 Ser Pro Lys Ile Phe Arg Pro Lys His Thr Arg Ile Ser Glu Leu Lys
 90            135                 140                 145
 92 gct gaa gca gtg aag aag gac cgc aga aag aag ctg acc cag tcc aag       535
 93 Ala Glu Ala Val Lys Lys Asp Arg Arg Lys Lys Leu Thr Gln Ser Lys
 94        150                 155                 160
 96 ttt gtc ggg gga gcc gag aac act gcc cac ccc cgg atc atc tct gca       583
 97 Phe Val Gly Gly Ala Glu Asn Thr Ala His Pro Arg Ile Ile Ser Ala
 98 165                 170                 175                 180
100 cct gag atg aga cag gag tct gag cag ggc ccc tgc cgc aga cac atg       631
101 Pro Glu Met Arg Gln Glu Ser Glu Gln Gly Pro Cys Arg Arg His Met
102                185                 190                 195
104 gag gct tcc ctg cag gag ctc aaa gcc agc cca cgc atg gtg ccc cgt       679
105 Glu Ala Ser Leu Gln Glu Leu Lys Ala Ser Pro Arg Met Val Pro Arg
106                200                 205                 210
108 gct gtg tac ctg ccc aat tgt gac cgc aaa gga ttc tac aag aga aag       727
109 Ala Val Tyr Leu Pro Asn Cys Asp Arg Lys Gly Phe Tyr Lys Arg Lys
110            215                 220                 225
112 cag tgc aaa cct tcc cgt ggc cgc aag cgt ggc atc tgc tgg tgc gtg       775
113 Gln Cys Lys Pro Ser Arg Gly Arg Lys Arg Gly Ile Cys Trp Cys Val
114        230                 235                 240
116 gac aag tac ggg atg aag ctg cca ggc atg gag tac gtt gac ggg gac       823
117 Asp Lys Tyr Gly Met Lys Leu Pro Gly Met Glu Tyr Val Asp Gly Asp
118 245                 250                 255                 260
120 ttt cag tgc cac acc ttc gac agc agc aac gtt gag tga tgcgtccccc       872
121 Phe Gln Cys His Thr Phe Asp Ser Ser Asn Val Glu
122                265                 270
123 cccaaccttt ccctcacccc ctcccacccc cagcccccgac tccagccagc ggctccctcc      942
126 acccccaggac gccactcatt tcatctcatt taaqqqaaaa atatatatct atctatttqa      962
128 qqaaactqaq qacctcqqaa tctctaqcaa qqqctcaact tcqaaaatqq caacaacaqa     1052
130 qatqcaaaaa qctaaaaaqa cacccccccc ctttaaatqq tttctttttt qaqqcaaqtt     1112
132 qqatqaacaq aqaaqqqaaq aqaqqaaqaa cqaqaqqaaq aqaaqqqaaq qaaqtqtttq     1172
134 tqtaqaaqaq aqaqaaaqac qaataqaqtt aqqaaaaqqa aqacaaqcaq qtqqqcaqqa     1232
136 aqqacatqca ccqaqaccaq qcaqqqqccc aactttcacq tccaqccctq qcctqqqqtc     1292
138 qqqaqaqqtq qqcqctaqaa qatqcaqccc aqqatqtqqc aatcaatqac actattqqqq     1352
140 tttcccaqqa tqqattqqtc aqqqqqaqaa aqqaaaaaqqc aaaacactcc aqqacctctc     1412
                                                                          1472
```

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```
144 ctcttacctg ggcagagtgt tgtctctccc caaatttata aaaactaaaa tgcattccat   1532
146 tcctctgaaa gcaaaacaaa ttcataattg agtgatatta aatagagagg ttttcggaag   1592
148 cagatctgtg aatatgaaat                                                1612
151 <210> SEQ ID NO  4
152 <211> LENGTH: 19
153 <212> TYPE: DNA
154 <213> ORGANISM: Artificial Sequence
156 <220> FEATURE:
158 <223> OTHER INFORMATION: PCR Primer
160 <400> SEQUENCE: 4
161 ccaaacacac ccgcatctc                                                 19
164 <210> SEQ ID NO: 5
165 <211> LENGTH: 22
166 <212> TYPE: DNA
167 <213> ORGANISM: Artificial Sequence
169 <220> FEATURE:
171 <223> OTHER INFORMATION: PCR Primer
173 <400> SEQUENCE: 5
174 ttggactggg tcagcttctt tc                                             22
177 <210> SEQ ID NO: 6
178 <211> LENGTH: 26
179 <212> TYPE: DNA
180 <213> ORGANISM: Artificial Sequence
182 <220> FEATURE:
184 <223> OTHER INFORMATION: PCR Probe
186 <400> SEQUENCE: 6
187 aggctgaagc agtgaagaag gaccgc                                         26
190 <210> SEQ ID NO: 7
191 <211> LENGTH: 19
192 <212> TYPE: DNA
193 <213> ORGANISM: Artificial Sequence
195 <220> FEATURE:
197 <223> OTHER INFORMATION: PCR Primer
199 <400> SEQUENCE: 7
200 gaaggtgaag gtcggagtc                                                 19
203 <210> SEQ ID NO: 8
204 <211> LENGTH: 20
205 <212> TYPE: DNA
206 <213> ORGANISM: Artificial Sequence
208 <220> FEATURE:
210 <223> OTHER INFORMATION: PCR Primer
212 <400> SEQUENCE: 8
213 gaagatggtg atgggatttc                                                20
216 <210> SEQ ID NO: 9
217 <211> LENGTH: 20
218 <212> TYPE: DNA
219 <213> ORGANISM: Artificial Sequence
221 <220> FEATURE:
223 <223> OTHER INFORMATION: PCR Probe
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PATENT APPLICATION: US/09/975,123   TIME: 08 41:48

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225 <400> SEQUENCE: 9
226 caagcttccc gttctcagcc                                          20
229 <210> SEQ ID NO: 10
230 <211> LENGTH: 1722
231 <212> TYPE: DNA
232 <213> ORGANISM: Homo sapiens
234 <220> FEATURE:
236 <220> FEATURE:
237 <221> NAME/KEY: CDS
238 <222> LOCATION: (752)...(1570)
240 <400> SEQUENCE: 10
241 gggaaaaga gctaggaaag agctgcaaag cagtgtgggc ttttttccctt ttttttgctcc    60
243 ttttcattac ccctcctccg ttttcaccct tctccggact tcgcgtagaa cctgcgaatt   120
245 tcgaagagga ggtggcaaag tgggagaaaa gaggtgttag ggtttggggt ttttttgttt   180
247 ttgtttttgt tttttaattt cttgatttca acattttctc ccaccctctc ggctgcagcc   240
249 aacgcctctt acctgttctg cggcgccgcg caccgctggc agctgagggt tagaaagcgg   300
251 gggtgtatttt agattttaag caaaaatttt aaagataaat ccattttttct ctcccacccc  360
253 caacgccatc tccactgcat ccgatctcat tatttcggtg gttgcttggg ggtgaacaat   420
255 tttgtggctt tttttcccct ataattctga cccgctcagg cttgagggtt tctccggcct   480
257 ccgctcactg cgtgcacctg gcgctgccct gcttccccca acctgttgca aggctttaat   540
259 tcttgcaact gggacctgct cgcaggcacc ccagccctcc acctctctct acattttgc    600
261 aagtgtctgg gggagggcac ctgctctacc tgccagaaat tttaaaacaa aaacaaaaac   660
263 aaaaaaatct ccggggggccc tcttggcccc tttatccctg cactctcgct ctcctgcccc  720
265 acccgaggt aaaggggggcg actaagagaa g atg gtg ttg ctc acc gcg gtc      772
266                                     Met Val Leu Leu Thr Ala Val
267                                      1               5
269 ctc ctg ctg ctg gcc gcc tat gcg ggg ccg gcc cag agc ctg ggc tcc   820
270 Leu Leu Leu Leu Ala Ala Tyr Ala Gly Pro Ala Gln Ser Leu Gly Ser
271            10              15              20
273 ttc gtg cac tgc gag ccc tgc gac gag aaa gcc ctc tcc atg tgc ccc   868
274 Phe Val His Cys Glu Pro Cys Asp Glu Lys Ala Leu Ser Met Cys Pro
275       25              30              35
277 ccc agc ccc ctg ggc tgc gag ctg gtc aag gag ccg ggc tgc ggc tgc   916
278 Pro Ser Pro Leu Gly Cys Glu Leu Val Lys Glu Pro Gly Cys Gly Cys
279 40              45              50              55
281 tgc atg acc tgc gcc ctg gcc gag ggg cag tcg tgc ggc gtc tac acc   964
282 Cys Met Thr Cys Ala Leu Ala Glu Gly Gln Ser Cys Gly Val Tyr Thr
283            60              65              70
285 gag cgc tgc gcc cag ggg ctg cgc tgc ctc ccc cag cag gac gag gag  1012
286 Glu Arg Cys Ala Gln Gly Leu Arg Cys Leu Pro Arg Gln Asp Glu Glu
287            75              80              85
289 aag ccg ctg cac gcc ctg ctg cac ggc cgc ggg gtt tgc ctc aac gaa  1060
290 Lys Pro Leu His Ala Leu Leu His Gly Arg Gly Val Cys Leu Asn Glu
291            90              95             100
293 aag agc tac cgc gag caa gtc aag atc gag aga gac tcc cgt gag cac  1108
294 Lys Ser Tyr Arg Glu Gln Val Lys Ile Glu Arg Asp Ser Arg Glu His
295       105             110             115
297 gag gag ccc acc acc tct gag atg gcc gag gag acc tac tcc ccc aag  1156
298 Glu Glu Pro Thr Thr Ser Glu Met Ala Glu Glu Thr Tyr Ser Pro Lys
```

```
299 120                     125                     130                     135
301 atc ttc cgg ccc aaa cac acc cgc atc tcc gag ctg aag gct gaa gca     1204
302 Ile Phe Arg Pro Lys His Thr Arg Ile Ser Glu Leu Lys Ala Glu Ala
303                 140                     145                     150
305 gtg aag aag gac cgc aga aag aag ctg acc cag tcc aag ttt gtc ggg     1252
306 Val Lys Lys Asp Arg Arg Lys Lys Leu Thr Gln Ser Lys Phe Val Gly
307             155                     160                     165
309 gga gcc gag aac act gcc cac ccc cgg atc atc tct gca cct gag atg     1300
310 Gly Ala Glu Asn Thr Ala His Pro Arg Ile Ile Ser Ala Pro Glu Met
311         170                     175                     180
313 aga cag gag tct gag cag ggc ccc tgc cgc aga cac atg gag gct tcc     1348
314 Arg Gln Glu Ser Glu Gln Gly Pro Cys Arg Arg His Met Glu Ala Ser
315     185                     190                     195
317 ctg cag gag ctc aaa gcc agc cca cgc atg gtg ccc cgt gct gtg tac     1396
318 Leu Gln Glu Leu Lys Ala Ser Pro Arg Met Val Pro Arg Ala Val Tyr
319 200                     205                     210                     215
321 ctg ccc aat tgt gac cgc aaa gga ttc tac aag aga aag cag tgc aaa     1444
322 Leu Pro Asn Cys Asp Arg Lys Gly Phe Tyr Lys Arg Lys Gln Cys Lys
323                 220                     225                     230
325 cct tcc cgt ggc cgc aag cgt ggc atc tgc tgg tgc gtg gac aag tac     1492
326 Pro Ser Arg Gly Arg Lys Arg Gly Ile Cys Trp Cys Val Asp Lys Tyr
327             235                     240                     245
329 ggg atg aag ctg cca ggc atg gag tac gtt gac ggg gac ttt cag tgc     1540
330 Gly Met Lys Leu Pro Gly Met Glu Tyr Val Asp Gly Asp Phe Gln Cys
331         250                     255                     260
333 cac acc ttc gac agc agc aac gtt gag tga tgcgtccccc cccaaccttt     1590
334 His Thr Phe Asp Ser Ser Asn Val Glu
335     265                     270
337 ccctcacccc ctcccacccc cagccccgac tccagccagc gcctccctcc accccaggac     1650
339 gccactcatt tcatctcatt taagggaaaa atatatatct atctatttga ggaaaaaaaa     1710
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341 aaaaaaaaaa aa
344 <210> SEQ ID NO: 11
345 <211> LENGTH: 21000
346 <212> TYPE: DNA
347 <213> ORGANISM: Homo sapiens
349 <220> FEATURE:
352 <400> SEQUENCE: 11
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355 gtcttccact ggcccctcca cctcctcccc attctcggta gccccagcct gtcccccttg     120
357 ccctttctt acattccggg gggaggaagg cgctgttcag agggggaggag ggcgctgttc     180
359 aggagcgaa gggagcccc cttgtgtcta gaaggcctct ccccacccc accccgtgtg     240
361 agtttgtact gcaaagctcc ttggcatcct tgcctgagtt gggtgtttggg aagctcaaat     300
363 tgcagctaca aactggctgg cagccagggg ccggctattt aaaagcgcct gctctcccgg     360
365 aggcccgtag tctctttgga aacttctgca gggaaaaga gctaggaaag agctgcaaag     420
367 cagtgtgggc ttttttcctt ttttgctcct tttcattacc cctcctccgt tttcaccctt     480
369 ctccggactt cgcgtagaac ctgcgaattt cgaagagcag gtggcaaagt gggagaaaag     540
371 aggtgttaggg gtttggggtt ttttgtttt tgttttgtt ttttaatttc ttgatttcaa     600
373 catttctcc caccctctcg gctgcagcca acgcctctta cctgttctgc ggcgccgcgc     660
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VERIFICATION SUMMARY   DATE   11/01/2001
PATENT APPLICATION: US/09/975,123   TIME   08:41 49

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date